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TTGGGACCCGCGAGGACACAGCAGCAGCTCAGGTGCTATGCTTGGGACCCGCGAGGACAGGCTGCCCCACCCGAGGCTCTTA 79

M L A G G V R 7
GAGGGCAGTCTGTTTGGCTTCTCAAGCCCATTTGACCCAGGTGAGCAGAGGG ATG CTG GCG GGG GGC GTG AGG 151

S M P S P L L A C W Q P I L L L V L G S 27
AGC ATG CCC AGC CCC CTC CTG GGC TGC TGG CAG CCC ATC CTC CTG CTG GTG CTG GGC TCA 211

V L S G S A T G C P P R C E C S A Q D R 47
GTG CTG TCA GGC TCG GCC ACG GGC TGC CTG CCC GGC TGC GAG TGC TCC GGC CAG GAC CTC 271

A V L C H R K R F V A V P E G I P T E T 57
GCT GTG CTG TGC CAC CGC AAG CGC TTT GTG GCA GTC CCC GAG GGC ATC CCC ACC GAG AGG 331

R L L D L G K N R I K T L N Q D E F A S 37
CGC CTG CTG GAC CTA GGC AAG AAC CGC ATC AAA ACG CTC AAC CAG GAC GAG TTC GCC AGC 391

F P H L E E L E L N E N I V S A V E P G 107
TTC CTG CAC CTG GAG GAG CTG GAG CTC AAC GAG AAC ATC GTG AGC GGC GTG GAG CCC GGC 451

A F N N L F N L R T L G L R S N R L K L 127
GCC TTC AAC AAC CTC TTC AAC CTC CGG ACG CTG GGT CTC CGC AGC AAC CGC CTG AAG CTC 511

I P L G V F T G L S N L T K L D T R E N 147
ATC CGC CTA GGC CTC TTC ACT GGC CTC AGC AAC CTG ACC AAG CTG GAC ACG AGG GAG AAC 571

K I V I L L D Y M F Q D L Y N L K S L E 167
AAG ATC GTT ATC CTA CTG GAC TAC ATG TTT CAG GAC CTG TAC AAC CTC AAG TCA CTG GAG 631

V G D N D L V Y I S H R A F S G L N S L 187
GTT GGC GAC AAT GAC CTC GTC TAC ATC TCT CAC CGC GGC TTC AGC GGC CTC AAC AGC CTG 691

E Q L T L E K C N L T S I P T E A L S H 207
GAG CAG CTG ACT CTG GAG AAA TGC AAC CTG ACC TCC ATC CCC ACC GAG GCG CTG TCC CAC 751

L H G L I V L R L R H L N I N A I R D Y 227
CTG CAC GGC CTC ATC GTC CTG AGG CTC CGG CAC CTC AAC ATC AAT GGC ATC CGG GAC TAC 811

S F K R L Y R L K V L E I S H W P Y L D 247
TCC TTC AAG AGG CTG TAC CGA CTC AAG GTC TTG GAG ATC TCC CAC TGG CCC TAC TTG GAC 871

T M T P N C L Y G L N L T S L S I T H C 267
ACC ATG ACA CCC AAC TGC CTC TAC GGC CTC AAC CTG ACG TCC CTG TCC ATC ACA CAC TCC 931

N L T A V P Y L A V R H L V Y L R F L N 287
AAT CTG ACC GCT GTG CCC TAC CTG GGC GTC CGC CAC CTA GTC TAT CTC CGC TTC CTC AAC 991

L S Y N P I S T I E G S M L H E L L R L 307
CTC TCC TAC AAC CCC ATC AGC ACC ATT GAG GGC TCC ATG TTG CAT GAG CTG CTC CGG CTG 1051

Q E I Q L V G G Q L A V V E P Y A F R G 327
CAG GAG ATC CAG CTG GTG GGC GCG CAG CTG GGC GTG GTG GAG CCC TAT GGC TTC CGC GGC 1111

L N Y L R V L N V S G N Q L T T L E E S 347
CTC AAC TAC CTG CGC GTG CTC AAT GTC TCT GGC AAC CAG CTG ACC ACA CTG GAG GAA TCA 1171

FIG. 1A

FIG. 1B

FIG. 2

Docket/Appl'n No.: 10/718,332
Title: Novel Genes Encoding Proteins ...
Inventors: Sean A. McCarthy, *et al.*
Replacement Sheet

Percent Similarity: 49.308 Percent Identity: 29.412

T79	1	MLAGGVRSMPSPLLACWQPILLVVGSVLSGS...ATGCPPRCECSAQDR.	47
D45913	1MARLSTGKAAC.QVVLGLLITSLTESSILTSECPQLCVCEIRPWF	44
T79	48AVLCHRKRFVAVPEGIPTETRLDLGKNRIKTLNQDEFAS	87
D45913	45	TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLLSNNI.....	84
T79	88	FPHLEELNENIVSAVEPGAFFNNLNFNLRTLGLRSNRLKLIPLGVFTGLS	137
D45913	85AKTVDELQQLFNLTELDIFSQNNFTNIKEVGLANLT	119
T79	138	NLTCLDTRENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNLSL	187
D45913	120	QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNOISTISANAFSGLKNL	169
T79	188	EQLTLEKCNLTISIPTALSHLHGLIVLRLRLHNLINAIIRDYSFKRLYRLKV	237
D45913	170	LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENFVIGILDMNFRPLSNLRS	219
T79	238	LEISHWPYLDTMTPNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL	286
D45913	220	LVLAG.MYLTDPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL	268
T79	287	NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY.....	323
D45913	269	DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDYALDNLPELTKE	318
T79	324AFRGLNYLRVLNVSGNQLTTLEESVFSVGNLETIL	360
D45913	319	ATNNPKLSYIHLAFRSVPALESMLNNALNAVYQKTVESLPNLREISI	368
T79	361	DSNPLACDCRLLWVFRWRRLNFRNQPT.CATPEFVQGKEFKDFPDVLL	409
D45913	369	HSNPLRCDVCVHWINSNKTNIREFMEPLSMFCAMPPEYRGQVK...EVLI	415
T79	410	PNYFT.CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKH	458
D45913	416	QDSSEQCLPMISHDTFPNHLNMDIGTTFLDCRAMAEPEPEIYWVTPIGN	465
T79	459	LVSAKS.NGRLTVPDGTLEVRYAQVQDNGTYLCIAANAGGNDSPAHLLH	507
D45913	466	KITVETLSDKYKLSSEGTEIANIQIEDSGRYTCVAQNVQADTRVATIK	515
T79	508	V.....RSYSPDWPHQ	518
D45913	516	VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN	565
T79	519	PNKTF.....AFISNQPGEGEANSTRA	540

FIG. 3A

045913 566 PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTK 615

T79 541 TVPFPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHIE 588

D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFKRNKYNHSL 665

T79 589 IEYVPRKSDAGISSADAPRKFNMKMI..... 614

D45913 666 KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714

FIG. 3B

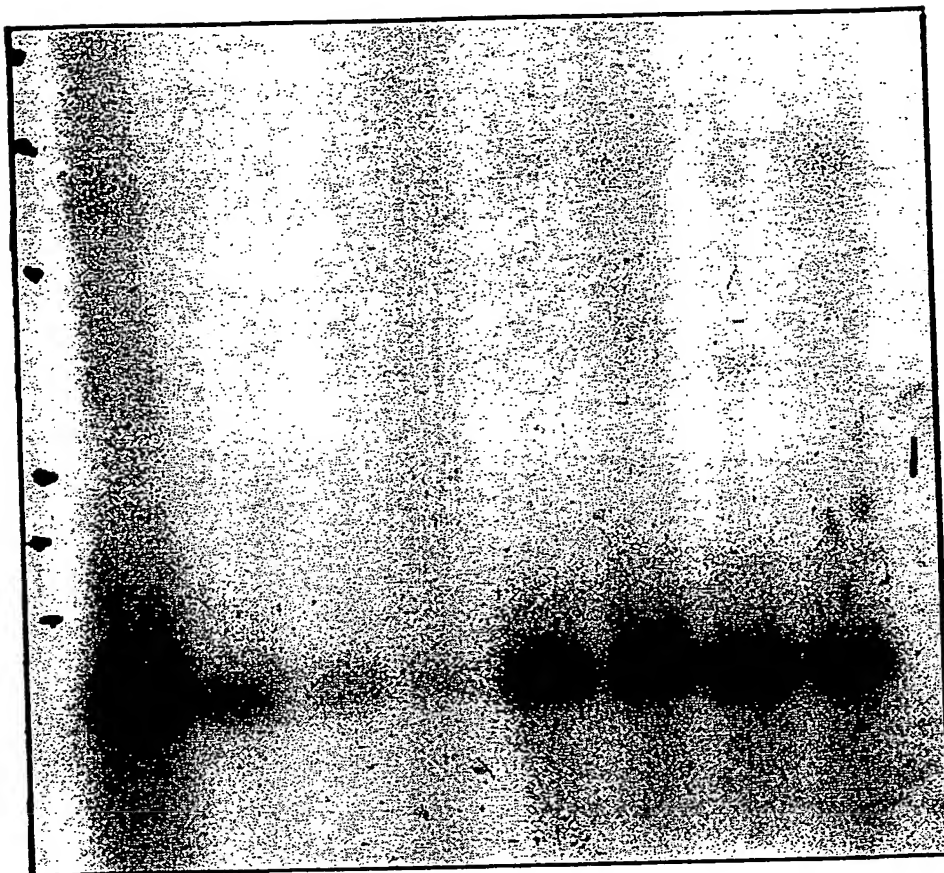


FIG. 4

T R P I L V I H D E Q K G P E V T S N	19
CC AGC CGT CCG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA GTG ACC TTC AAT	59
A A L T L R N F C N W Q K Q H N P P S D	39
GCT GCC CTC ACT CTG CCG AAC TTT TGC AAC TGG CAG AAG CAG CAC AAC CCA CCC AGT GAC	119
R D A E H Y D T A I L F T R Q D L C G S	59
CCG GAT GCA GAG CAC TAT GAC ACA GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC	179
Q T C D T L G M A D V G T V C D P S R S	79
CAG ACA TGT GAT ACT CTT GGG ATG GGT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC	239
C S V I E D D G L Q A A F T T A H E L G	99
TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC CAT GAA TTA GGC	299
H V F N M P H D D A K Q C A S L N G V N	119
CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG TGT GCC AGC CTT AAT GGT GTG AAC	359
Q D S H M M A S M L S N L D H S Q P W S	139
CAG GAT TCC CAC ATG ATG GCG TCA ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT	419
P C S A Y M I T S F L D N G H G E C L M	159
CCT TCC AGT GCC TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG	479
D K P Q N P I Q L P G D L P G T S Y D A	179
GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CTT GGC ACC TCG TAC GAT GCC	539
N R Q C Q F T F G E D S K H C P D A A S	199
AAC CCG CAG TCC CAG TTT ACA TTT GGG GAG GAC TCC AAA CAC TCC CCT GAT GCA GCC AGC	599
T C S T L W C T G T S G G V L V C Q T K	219
ACA TGT AGC ACC TTG TGG TGT ACC GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA	659
H F P W A D G T S C G E G K W C I N G K	239
CAC TTC CCG TGG GCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GCC AAG	719
C V N K T D R K H F D T P F H G S W G M	259
TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT ACG CTT TTT CAT GGA AGC TGG GGA ATG	779
W G P W G D C S R T C G G G V Q Y T M R	279
TGG GGG CCT TGG GGA GAC TGT TCG AGA ACG TGC GGT GGA GGA GTC CAG TAC ACG ATG AGG	839
E C D N P V P K N G G K Y C E G K R V R	299
GAA TGT GAC AAC CCA GTC CCA AAG AAT GGA GGG AAG TAC TGT GAA GGC AAA CCA GTG CCG	899
Y R S C N L E D C P D N N G K T F R E E	319
TAC AGA TCC TGT AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA	959
Q C E A H N E F S K A S F G S G P A V E	339
CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG CCT GCG GTG GAA	1019
W I P K Y A G V S P K D R C K L I C Q A	359
TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC AGG TGC AAG CTC ATC TGC CAA GCC	1079
K G I G Y F F V L Q P K V V D G T P C S	379
AAA GGC ATT GGC TAC TTC TTC GTT TTG CAG CCC AAG GTT GTA GAT GGT ACT CCA TGT AGC	1139

FIG. 5A

Docket/Appl'n No.: 10/718,332
 Title: Novel Genes Encoding Proteins ...
 Inventors: Sean A. McCarthy, *et al.*
 Replacement Sheet

P D S T S V C V Q G Q C V K A G C D R I	399
CCA GAT TCC ACC TCT GTC TOT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CCG ATC	1199
I D S K K K F D K C G V C G G N G S T C	419
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TOC GGG GGA AAT GGA TCT ACT TGT	1259
K K I S G S V T S A K P G Y H D I I T I	439
AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT	1319
P T G A T N E E V K Q R N Q R G S R N N	459
CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CCG AAC CAG AGG GGA TCC AGG AAC AAT	1379
G S F L A I K A A D G T Y I L N G D Y T	479
GGC ACC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT	1439
L S T L E Q D I M Y K G V V L R Y S G S	499
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GCC TCC	1499
S A A L E R I R S F S P L K E P L T I Q	519
TCT CGC GCA TTG GAA AGA ATT CCG AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG	1559
V L T V G N A L R P K I K Y T Y F V K K	539
GTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTG GTA AAG AAG	1619
K K E S F N A I P T F S A W V I E E W G	559
AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC	1679
E C S K T C G K G Y K K R S L K C L S H	579
GAA TGT TCT AAG ACC TGT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT	1739
D G G V L S H E S C D P L K K P K H F I	599
GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CTT AAA CAT TTC ATA	1799
D F C T M A E C S *	609
GAC TTT TCC ACA ATG GCA GAA TCC AGT TAA	1829
GTGGTTTAAGTGGTGTAGCTCTGAGGGCAAGGCCAAGTGGGAAGGGCTGGTCCAGGAAAGCAAGAGGGCTGGAGGG	1908
ATCCAGGCTATCTTCCAGTAACCACTGAGGTGTATCAGTAAGGTGGGATTATGGGGGTAGATAGAAAAGGAGTTGAAT	1987
CATCAGAGTAAGTCCCACTTCCAAAATTTCTAGGATAGTTAGTGAGGATTATTAACCTCTGAGCAGTGATATAGCATA	2066
ATAAAGGCCCCGGCAATTATATATATTTCTTTTGTACATCTATTACAAGTTTGGAAAAACAAGCAATTGTCAA	2145
AAAAGTTAGAACTATTACAACCCCTGTTTCTGTTACTTATCAATACTTAGTATCATGGGGGTGGGAATGAAAAGT	2224
AGGAGAAAAGTGAGATTTTACTAAGACCTGTTTACTTTACTCTACTAACAATGGGGGAGAAAGGATACAATAGGA	2303
TCCTTGACCGCACTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCTACCGAGAATTAAACTTCA	2382
GATTGTTCAACATGAGAGAAAGGCTCAGCAACGTGAATAACGCCAATGGCTTCTCTTTCTTTTCTTTTGGACCTCTCA	2461
GTCTTTATTTGTGTAATTCATTTTGAGGAAAAACAACCTCCATGTATTATTCAAGTGCATTAAAGTCTCAATGGAAA	2540
AAAAGCAGTGAGCATTAGATGCTGTTAAAGCTAGAGGAGACACAATGAGCTTGTACCTCCACTTCTTTCTTTTCTC	2619
TACCATGTAAACCTGCTTTTGGGAATATGGATGTAAAGAAGTAACTTGTGTCTCATGAAAATCAGTACAATCACACAAGG	2698

FIG. 5B

AGGATGAAACGCCCGACAAAAATGAGGTGTGTGACACGGTCTGCTGAGTTTGGGACATTGAGATCAGTTTCTTTG 2777
TGGTGGGGAAGGTTGCTGAGGTTACAGGTCTCTCTCGGAGCTGGTCCGACAGTGGATTCCTGGTGAATGCTGTTG 2856
AGCTCTTGTGTGAGAAATATGATTTTTTCCGATGTATATAGTAAATATGTTACCTATAATTACATGTACTTTTAAAT 2935
ATTGCTTTGGGTGTTCCTTCCGAGAAGGACTATAGTTAGTAATAAATGCCCTATAATAACATATTTATTTTATACATT 3014
ATTCTAATGAAAAAAGCTTTTAAATTATATCGCTTTTGTGGAAGTCCATATAAATAGAGTATTTATACAAATATGT 3093
TACTAGAAATAAAAGAACACTTTTGGAAAAAAGGGCGGGCCG 3147

FIG. 5C

```

251 DQSMADFHSSGLKAYLLTLFSAARFYKHPSTIRNSISLVVVKILVTYEEQ 300
      ||||:|
1 .....TRPILVTRDEQ 11

301 KGPEVTSNAALTILNFCSSWQKQHNSPDRDPHYDTAILFTRODLGGSHT 350
      |||||:|
12 KGPEVTSNAALTILNFCSSWQKQHNSPDRDAERYDTAILFTRODLGGSQT 61

351 CDTLGMADVGTVCDFSRSCSVTEDDGLQAAFTTABELGHVFNMPHDDAKH 400
      |||||:|
62 CDTLGMADVGTVCDFSRSCSVTEDDGLQAAFTTABELGHVFNMPHDDAKQ 111

401 CASLNGVSGDSHLMASMLSSLCHSQFWSPCSAYMVTSLDNGHGECIMDK 450
      |||||:|
112 CASLNGVSGDSHLMASMLSSLCHSQFWSPCSAYMVTSLDNGHGECIMDK 161

451 PQNPILPDLPGTLYDANRQCQFTFGEDSKHCPDAASTCTLNCTGTSG 500
      |||||:|
162 PQNPILPDLPGTLYDANRQCQFTFGEDSKHCPDAASTCTLNCTGTSG 211

501 GLLVCQTKHFPAWAGTSCGEGKWCVSGKCVNKTDMKHFATFVHGSNGPWG 550
      |||||:|
212 GLLVCQTKHFPAWAGTSCGEGKWCVSGKCVNKTDMKHFATFVHGSNGPWG 261

551 PWGDCSRTCCGGVQYTMRECNFVFKNGGKYCEGKRVRYRSCNLEDCPDN 600
      |||||:|
262 PWGDCSRTCCGGVQYTMRECNFVFKNGGKYCEGKRVRYRSCNLEDCPDN 311

601 NGKTFREEQCEAHNEFSKASFGNEPTVETPKAGVSPKDRCKLTCEANG 650
      |||||:|
312 NGKTFREEQCEAHNEFSKASFGSGPAVENTPKAGVSPKDRCKLTCEANG 361

651 IGYFFVLQPKVVDGTPCSPDSTSVCVQGCQVKAGCDRIIDSKKKFDRQGV 700
      |||||:|
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGCQVKAGCDRIIDSKKKFDRQGV 411

701 CCGNGSTCKRMMSGIVTSTRPGYHDIITIPGATNIEVKRNQRGSRNGS 750
      |||||:|
412 CCGNGSTCKRMMSGIVTSTRPGYHDIITIPGATNIEVKRNQRGSRNGS 461

751 FLAIRAADGTYTLNGFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 800
      |||||:|
462 FLAIRAADGTYTLNGFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLAVGHALRPKIDFTYFMKKKTESFNAIPTFSWVDEWGE 850
      |||||:|
512 LKEPLTIQVLAVGHALRPKIDFTYFMKKKTESFNAIPTFSWVDEWGE. 560

901 WSPCSKTCKGKYKRLKCVSHDGGVLSNESCDPLKPKHYIDFCTLTC 950
      |||||:|
561 ...CSKTCKGKYKRLKCVSHDGGVLSNESCDPLKPKHYIDFCTLTC 607

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951 S* 951
|
608 S* 609

FIG. 6

Docket/App'l'n No.: 10/718,332
Title: Novel Genes Encoding Proteins ...
Inventors: Sean A. McCarthy, *et al.*
Replacement Sheet

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg	50
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu	
1 5 10	
atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt	98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly	
15 20 25 30	
acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa	146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu	
35 40 45	
tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc	194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys	
50 55 60	
act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct	242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro	
65 70 75	
tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc	290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly	
80 85 90	
aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat	338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His	
95 100 105 110	
gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt	386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys	
115 120 125	
ggg ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca	434
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro	
130 135 140	
aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc	482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser	
145 150 155	
tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag	530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu	
160 165 170	
gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat	578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn	
175 180 185 190	
gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tgc cca aag	626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys	
195 200 205	

FIG. 7A

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

FIG. 7B

Replacement Sheet

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg 1298
 Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
 115 420 425 430

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346
 Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
 435 440 445

gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394
 Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
 450 455 460

tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442
 Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
 465 470 475

tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490
 Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
 480 485 490

tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538
 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
 495 500 505 510

ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592
 Phe Cys Thr Leu Thr Gln Cys Ser
 515

ggagggggctg atacactgag tgcaagagta ctggaggggat ccagtgagtc aaaccagtaa 1652
 gcagtgaggt gtggcaagga ggtgtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712
 acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772
 gaccatacag agcactaagg agccccaagg cactattagt atctcttttc ttatatctat 1832
 cgcccaaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt 1892
 cttatcacaa agattgggaa aggcaaagca gaaagatggg aagactgggt ttcaaacaag 1952
 gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
 gctgggttgc gtggtttttac ggaagggttg tgcattcatt ctatcaacag tgaaaagttc 2072
 agcttggtca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132
 accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa 2192
 atgtacattg gaaaaaaaaa gtgaagttta tgaggtacac ataaaaactg aaggaaacaa 2252
 tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt 2312
 gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta 2372
 gaatggggta tagagatcag ggtcccatga gatggggaac atgggtgatca ctcatctcac 2432
 atgggaggct gctgcagggt agcagggtcca ctctggcag ctggtccaac agtcgtatcc 2492
 tggatgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat 2552
 gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt 2612
 tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata 2672
 catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
 atagagtatt tatacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792
 atgcctatatt tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat 2852
 tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt 2912
 actaataaaa aagaagttga tgatgtcttt agtggttaaga ttgttactaa tgtggttggc 2972
 aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttctgcc 3032
 acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat 3092
 gataaactgt ggctgtgctt taataaaact ttattttacaa aaaaaaaaaa aaa 3145

FIG. 7C

cgggccgctc	ccggccggcc	caagggacag	agccaggctc	cgggagccc	caacactcgt	60
cttgagagcc	ccggctcctc	agcccgcctac	ggccaggggc	tcggcctccg	cccccgactc	120
ccgagctcct	gccctagagt	cgactgggct	cccggccgcg	tgggacagac	agacggacag	180
ccagccctgc	gagggcgcg	ggaccggg	gaggtgtgt	aggaggagac	cgaggagggg	240
ggctgggctg	gggctggggc	cgcgccggca	agagagacat	gcgattggtg	accaagccga	300
gcggacggac	agcgcgccc	ag atg cag	gtg agc gag	agg atg ctg	gca ggg	352
		Met Gln Val Ser Glu Arg Met Leu Ala Gly				
		1		5		10
ggg atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc						400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile						
	15		20		25	
ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc						448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys						
	30		35		40	
ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac						496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His						
	45		50		55	
cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc						544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg						
	60		65		70	
ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag						592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu						
	75		80		85	90
ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc						640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile						
	95		100		105	
gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg						688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg						
	110		115		120	
act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc						736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val						
	125		130		135	
ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag						784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys						
	140		145		150	
atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag						832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys						
	155		160		165	170
tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc						880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala						
	175		180		185	

FIG. 8A

Docket/Appl'n No.: 10/718,332
Title: Novel Genes Encoding Proteins ...
Inventors: Sean A. McCarthy, *et al.*
Replacement Sheet

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn	
190 195 200	
ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile	
205 210 215	
gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc	1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser	
220 225 230	
ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro	
235 240 245 250	
tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser	
255 260	

FIG. 8B


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ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
ttgacagcca gtccgcccgt ccggagcccg gctcgttggg gcagc atg gcg ggg tcg 117
                                     Met Ala Gly Ser
                                     1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
  5                10                15                20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
      25                30                35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
      40                45                50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
      55                60                65

gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
      70                75                80

gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
      85                90                95                100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
      105                110                115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
      120                125                130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
      135                140                145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
      150                155                160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
      165                175

atcctcaccg gaagttcgga gccagaggct gctcctgccc cgcgccgcct ccgccgatct 710
gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
gtcaaacgcc tggagaaccc ctgcgccag gcgcggcac gccgcctct gctcctctga 830

```

FIG. 9A



Docket/App'l'n No.: 10/718,332
Title: Novel Genes Encoding Proteins ...
Inventors: Sean A. McCarthy, *et al.*
Replacement Sheet

```
gcgotgctgc atcctgcacg ccctggaacc caggagcgcc ccagcaaccc tgactccctg 890
ccagcacgtc caaggctgct taccccagca acctcccatc ccctgagccc tcaataaatg 950
ccatctgtag caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
aaaaaaaaaa aaaaaaaa
```

FIG. 9B